

## SEQUENCE LISTING

<110> Hong Zhang  
Andrew T. Watt

<120> ANTISENSE MODULATION OF CASPASE 7 EXPRESSION

<130> RTS-0201

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Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn  
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qta att tat ggg aaa gat ggt gtc aca cca ata aag gat ttg aca gcc 535

Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys Asp Leu Thr Ala  
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&lt;223&gt; PCR Primer

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&lt;210&gt; 9

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Probe

&lt;400&gt; 9

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21

&lt;210&gt; 10

&lt;211&gt; 2006

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&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (474) ... (1496)

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cctacaaatc ttaaagtagc tccatcaaat ctgcagtttt cacattattg aaaatgtctg 240

tcacataggt acaaatttag aatcatcaca ttatattaca tggctattct aggtcatcta 300

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ccc tcg acc ctt gcg gag gac gga cgc tgc cgt ggg ctc ctg gcc gcc	572
Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala	
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aag gtg gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc	668
Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg	
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Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr	
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Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys	
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Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys	
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<210> 12

<211> 23

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Met Ala Asp Asp Gln Gly Cys Ile Glu

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Pro Asp Arg Ser Ser Phe Val Pro Ser Leu Phe Ser Lys Lys Lys Lys

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Leu Leu Lys Lys Ala Ser Glu Glu Asp His Thr Asn Ala Ala Cys Phe	
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Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn Val Ile Tyr Gly Lys	
140 145 150	
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RTS-0201

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gtt ggt tgg cct cca ggc agg aag tgg cac ttg gaa aag aac acc agc 285  
 Val Gly Trp Pro Pro Gly Arg Lys Trp His Leu Glu Lys Asn Thr Ser  
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RTS-0201-14-PATENT

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Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile Lys Thr  
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acc cgg gac cga gtg cct aca tat cag tac aac atg aat ttt gaa aag 525  
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85 90 95

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100 105 110 115

ggt atg ggc gtt cga aac gga aca gac aaa gat gcc gag gcg ctc ttc 621  
Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala Leu Phe  
120 125 130

aag tgc ttc cga agc ctg ggt ttt gac gtg att gtc tat aat gac tgc 669  
Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn Asp Cys  
135 140 145

tct tgt gcc aag atg caa gat ctg ctt aaa aaa gct tct gaa gag gac 717  
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150 155 160

cat aca aat gcc gcc tgc ttc gcc tgc atc ctc tta agc cat gga gaa 765  
His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His Gly Glu  
165 170 175

gaa aat gta att tat ggg aaa gat ggt gtc aca cca ata aag gat ttg 813  
Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys Asp Leu  
180 185 190 195

aca gcc cac ttt agg ggg gat aga tgc aaa acc ctt tta gag aaa ccc 861  
Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu Lys Pro  
200 205 210

aaa ctc ttc ttc att cag gct tgc cga ggg acc gag ctt gat gat ggc	909
Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Asp Gly	
215 220 225	
atc cag gcc gac tcg ggg ccc atc aat gac aca gat gct aat cct cga	957
Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn Pro Arg	
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Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser Thr Val	
245 250 255	
cca ggc tat tac tca tgg agg agc cca gga aga ggc tcc tgg ttt gtg	1053
Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val	
260 265 270 275	
caa gcc ctc tgc tcc atc ctg gag gag cac gga aaa gac ctg gaa atc	1101
Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu Glu Ile	
280 285 290	
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Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys	
310 315 320	
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Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln	
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&lt;211&gt; 2378

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (147) ... (908)

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ggcccgaagc ggatcagcct tgtggg atg gca gat gat cag ggc tgt att gaa 173  
Met Ala Asp Asp Gln Gly Cys Ile Glu

1

5

gag cag ggg gtt gag gat tca gca aat gaa gat tca gtg gat gct aag 221  
Glu Gln Gly Val Glu Asp Ser Ala Asn Glu Asp Ser Val Asp Ala Lys  
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Pro Asp Arg Ser Ser Phe Val Pro Ser Leu Phe Ser Lys Lys Lys Lys  
30 35 40aat gtc acc atg cga tcc atc aag acc acc cgg gac cga gtg cct aca 317  
Asn Val Thr Met Arg Ser Ile Lys Thr Thr Arg Asp Arg Val Pro Thr  
45 50 55tat cag tac aac atg aat ttt gaa aag ctg ggc aaa tgc atc ata ata 365  
Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly Lys Cys Ile Ile Ile  
60 65 70aac aac aag aac ttt gat aaa gtg aca ggt atg ggc gtt cga aac gga 413  
Asn Asn Lys Asn Phe Asp Lys Val Thr Gly Met Gly Val Arg Asn Gly  
75 80 85aca gac aaa gat gcc gag gcg ctc ttc aag tgc ttc cga agc ctg ggt 461  
Thr Asp Lys Asp Ala Glu Ala Leu Phe Lys Cys Phe Arg Ser Leu Gly  
90 95 100 105ttt gac gtg att gtc tat aat gac tgc tct tgt gcc aag atg caa gat 509  
Phe Asp Val Ile Val Tyr Asn Asp Cys Ser Cys Ala Lys Met Gln Asp  
110 115 120ctg ctt aaa aaa gct tct gaa gag gac cat aca aat gcc gcc tgc ttc 557  
Leu Leu Lys Lys Ala Ser Glu Glu Asp His Thr Asn Ala Ala Cys Phe  
125 130 135gcc tgc atc ctc tta agc cat gga gaa gaa aat atg gaa tct tgc tct 605  
Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn Met Glu Ser Cys Ser  
140 145 150

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Pro Pro Pro Arg Leu Ala Glu Gly Pro Ser Leu Met Met Ala Ser Arg	
170 175 180 185	
ccg act cgg ggc cca tca atg aca cag atg cta atc ctc gat aca aga	749
Pro Thr Arg Gly Pro Ser Met Thr Gln Met Leu Ile Leu Asp Thr Arg	
190 195 200	
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Ser Gln Trp Lys Leu Thr Ser Ser Ser Pro Ile Pro Arg Phe Gln Ala	
205 210 215	
att act cgt gga gga gcc cag gaa gag gct cct ggt ttg tgc aag ccc	845
Ile Thr Arg Gly Gly Ala Gln Glu Glu Ala Pro Gly Leu Cys Lys Pro	
220 225 230	
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Ser Ala Pro Ser Trp Arg Ser Thr Glu Lys Thr Trp Lys Ser Cys Arg	
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Ser Ser Pro Gly	
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&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; Antisense Oligonucleotide

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<223> Antisense Oligonucleotide

<400> 25

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<210> 30

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<210> 37  
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<223> Antisense Oligonucleotide

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acattctgca ataaagagca

20

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<223> Antisense Oligonucleotide

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<210> 87  
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ccaaagctgc cctcgaccct tgcggaggac ggacgctgcc gtgggctcct ggccgcccgc	180
gtgggaacg atg acc gat gat cag gac tgt gct gcg gag ctg gaa aag gtg	231
Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu Lys Val	
1 5 10	
gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc tcc tct	279
Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg Ser Ser	
15 20 25 30	
atc atc tcc tct att ctc ttg aag aag aag aga aat gcc tct gcg ggc	327
Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser Ala Gly	
35 40 45	
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Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr Arg Met	
50 55 60	
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Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe	
65 70 75	
gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa gat gca	471
Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys Asp Ala	
80 85 90	
ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta acc gtc	519
Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val Thr Val	
95 100 105 110	



cac aat gac tgc tct tgt gca aag atg caa gat ctg ctt aga aaa gcc 567  
 His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg Lys Ala  
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 Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val Thr Pro  
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